REMARKS

Reconsideration of this application is requested in view of the amendments to the claims and the remarks presented herein.

The claims in the application are claims 26 to 32, all other claims having been cancelled.

The Examiner indicated that claims 11 to 15, 18 and 19 were free of the prior art and the present claims 26 to 30 correspond to these claims. The objected to expression "DNA bank" has been changed to "DNA sample" as suggested by the Examiner. The expression "identification of the precursor" has been clarified to make clear that it is the non-amidified precursor. Therefore, it is believed that the claims in the application are allowable.

In view of the amendments to the claims and the above remarks, it is believed that the claims clearly point out Applicants' patentable contribution and favorable reconsideration of the application is requested.

Respectfully submitted,
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CAM:ds
Enclosures

MARKED UP VERSION OF CLAIMS

Our Ref.: 427.034

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: :
MARTINEZ et al : Examiner: J. Taylor
Serial No.: 09/486,142 :
Filed: March 31, 2000 : Group: 1656
For: OLIGONUCLEOTIDES...HORMONES :

600 Third Avenue
New York, NY 10016
Dated:

AMENDMENT

Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

Responsive to the Office Action of ~~October 4~~ May 15, 2001, please amend this application as follows:

IN THE CLAIMS:

Cancel claims 1 to 25 and add the following claims.

--26. A single-stranded oligonucleotide OX comprising 9 to 42 nucleotides and hybridizes under mild conditions with an oligonucleotide OY of the sequence Y_1-Y_2-Y_3-Y_4-Y_5 wherein Y_1 is a nucleotide sequence of 1 to 12 nucleotides or is absent, Y_2 is a trinucleotide which codes for Gly, Y_3 is a nucleotide coding for Arg or Lys, R_4 is a nucleotide coding for Arg or Lys and Y_5 is a nucleotide sequence of 1 to 21 nucleotides or is absent.

~~33~~ 26. A single stranded oligonucleotide OY comprising 9 to 42 nucleotides of the sequence Y_1-Y_2-Y_3-Y_4-Y_5 wherein Y_1 is a nucleotide sequence of 1 to 12 nucleotides or is absent, Y_2 is a trinucleotide which codes for Gly, Y_3 is a nucleotide coding for Arg or Lys, R_4 is a nucleotide coding for Arg or Lys and Y_5 is a nucleotide sequence ~~of 1 to 21 nucleotides or is absent~~.

34. An oligonucleotide OY of claim 33 wherein Y_1 is absent.

35. An oligonucleotide OY of claim 33 wherein Y_5 is absent.

36. An oligonucleotide OY of claim 33 wherein Y_5 is a nucleotide sequence Y_6-Y_7-Y_8-Y_9 wherein Y_6 is a trinucleotide which codes for Ser, Thr or Tyr, Y_7 is a trinucleotide which codes for any amino acid, Y_8 is a trinucleotide which codes for Glu or Asp and Y_9 is a nucleotide sequence of 1 to 12 nucleotides or is absent.

~~2~~7. An oligonucleotide of claim ~~3~~6 wherein Y_1 and Y_9 are absent.

~~2~~8. An oligonucleotide ~~OX~~ OY of claim ~~2~~7 ~~which hybridizes with OY~~ wherein Y_2 is a trinucleotide which codes for Gly, Y_3 is a trinucleotide which codes for Lys, Y_4 is a trinucleotide which codes for Arg and Y_5 is a sequence of 3 trinucleotides which code for Ser-Ala-Glu.

29. A single-stranded oligonucleotide OZ comprising 15 to 39 nucleotides and hybridizes under mild or stringent conditions with a consensus signal sequence characteristic of amidated polypeptide hormones with the sequence having the formula

$$Z_1-Z_2-Z_3-Z_4-Z_5-Z_6-Z_7$$

wherein Z_1 is a nucleotide sequence of 1 to 12 nucleotides or is absent, Z_2 and Z_3 are two trinucleotides which code for Leu, Z_4 and Z_5 are two trinucleotides which code for any two amino acids, Z_6 is a trinucleotide which codes for Leu and Z_7 is a nucleotide sequence of 1 to 12 nucleotides or is absent.

40. A group of oligonucleotides OX of claim 26 which constitute a combinational library.

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41. A group of oligonucleotides OZ of claim 29 which constitute a combinational library.

42. A method of identifying the precursor of a peptide having an amidated C-terminal end comprising 1) obtaining a DNA sample, 2) hybridizing at least one oligonucleotide of claim 26 with the DNA sample, 3) identifying the DNA sequence(s) of the DNA sample hybridized with the oligonucleotide(s) of claim 26 and (4) identifying in this sequence at least one precursor of peptides with an optional amidated C-terminal end.

43. A method of identifying the precursor of a peptide having

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~~49~~. A method for identifying the non-amidated precursor of a peptide having an amidated C-terminal end comprising 1) obtaining a DNA sample, 2) amplifying the fragment of interest by PCR technique with a group of oligonucleotides of claim 26, 3) identifying the DNA sequence(s) of the DNA sample which hybridize with the oligonucleotide of claim 26 and 4) identifying in the sequence(s) of at least one non-amidated precursor of peptides with an optional amidated C-terminal end.

32 31

~~50~~. The method of claim ~~48~~ wherein the amplification is effected with a combinational library of claim 30.

51. The method of claim 49 wherein the amplification is effected with a combinational library of claim 40.

52. A method of identifying the precursor of a polypeptide having an amidated C-terminal end comprising 1) obtaining a DNA sample, 2) amplifying the fragment of interest by PCR technique with an oligonucleotide of claim 26 and a second single-stranded oligonucleotide which hybridizes under mild or stringent conditions with a universal consensus sequence contained in the sequence of the plasmid vector in which the cDNA of the DNA sample are cloned, 3) identifying the DNA sequence of the DNA sample which hybridizes with an oligonucleotide of claim 26 and 4) identifying in the sequence at least one precursor of peptides with an optional amidated C-terminal end.